

Package: epp (via r-universe)

June 2, 2026

Title R Implementation of the EPP model for HIV epidemic estimates.

Version 0.4.4

Description This implements the EPP r-spline and r-trend models for HIV epidemic estimates.

Depends R (>= 3.1.0)

License GPL-3

Encoding UTF-8

LazyData true

Imports mvtnorm, anclik (>= 0.3), xml2

Remotes jeff Eaton/anclik

RoxygenNote 7.2.3

Config/pak/sysreqs libxml2-dev

Repository <https://mrc-ide.r-universe.dev>

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RemoteUrl <https://github.com/jeff Eaton/epp>

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<code>.parse_array</code>	<i>Parse java array from EPP .xml file</i>
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Description

Parse java array from EPP .xml file

Usage

```
.parse_array(x)
```

Arguments

x	'xml_node' object with tag 'array'
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<code>.parse_matrix</code>	<i>Parse java matrix from EPP .xml file</i>
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Description

Parse java matrix from EPP .xml file

Usage

```
.parse_matrix(x)
```

Arguments

x	'xml_node' object with tag 'array' and type '[D' or '[I'
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<code>get_eppxml_workset</code>	<i>Return workset with names from EPP .xml file</i>
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Description

Return workset with names from EPP .xml file

Usage

```
get_eppxml_workset(pjnz)
```

Arguments

x	'xml_node' object with tag 'array'
---	------------------------------------

```
prepare_ancsite_likdat
```

Prepare site-level ANC prevalence data for EPP random-effects likelihood

Description

Prepare site-level ANC prevalence data for EPP random-effects likelihood

Usage

```
prepare_ancsite_likdat(eppd, anchor.year = 1970L)
```

Arguments

eppd	EPP data object
anchor.year	year in which EPP data inputs start NOTE: requires year to be stored in column names of anc.prev

```
read_epp_data
```

Read EPP fitting surveillance data

Description

Reads the HIV prevalence from sentinel surveillance and household surveillance data from the EPP .xml file within a PJNZ.

Usage

```
read_epp_data(pjnz)
```

Arguments

pjnz	file path to Spectrum PJNZ file.
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Details

EPP projection sets are identified in the .xml file by searching the XML tree for tag "object", and then selecting objects with "class" attribute equal to "epp2011.core.sets.ProjectionSet".

read_epp_subpops *Read EPP subpopulation configuration*

Description

Reads the subpopulation configuration and population sizes from the EPP .xml file within a PJNZ.

Usage

read_epp_subpops(pjnz)

Arguments

pjnz file path to Spectrum PJNZ file.

Details

EPP projection sets are identified in the .xml file by searching the XML tree for tag "object", and then selecting objects with "class" attribute equal to "epp2011.core.sets.ProjectionSet".

read_epp_workset_options
Read EPP Workset Options

Description

Parse 'Worset option' selections for overall EPP workset in the "Model options" pop up box in the Curve Fitting workflow

Usage

read_epp_workset_options(pjnz)

Arguments

pjnz file path to Spectrum PJNZ file

`read_eppxml_results` *Read Bayesian Median outputs from XML*

Description

Read Bayesian Median outputs from XML

Usage

`read_eppxml_results(pjnz)`

Arguments

`pjnz`

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